

63247007

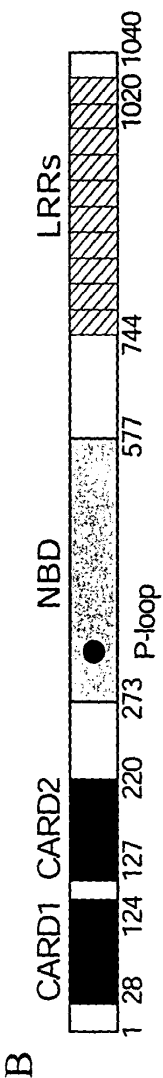
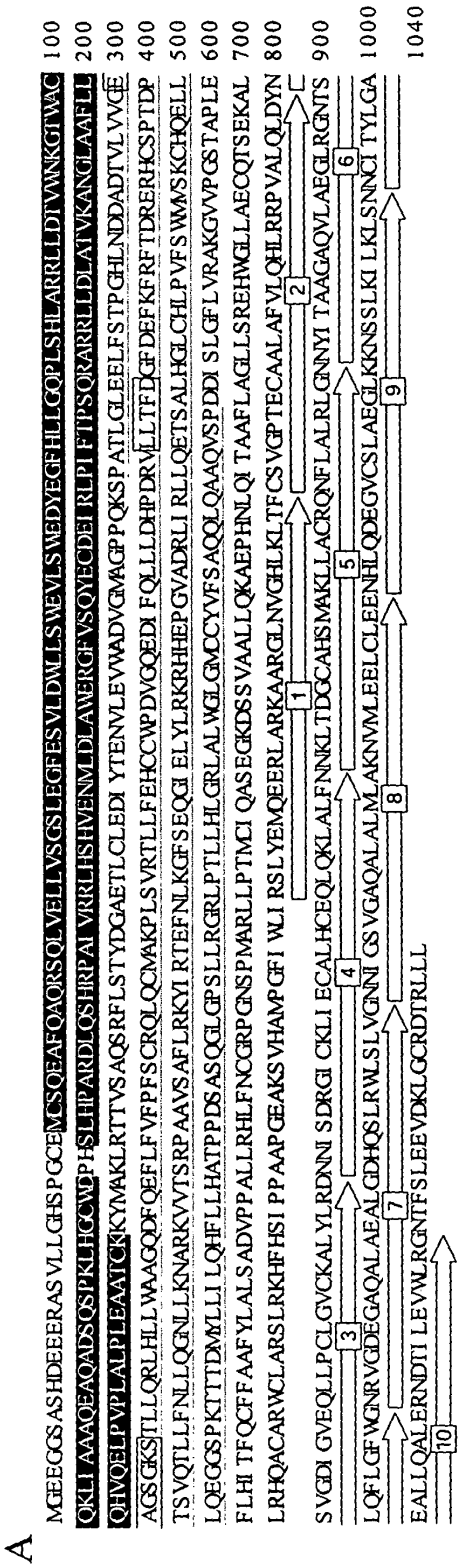


Figure 1

A

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Nod2(2)	127	SEEP-AGDQOSRRPATVRRTHSHV---ENMDLAWEGFVSQMECDERPIET-PSQARRLLDQATVKNGLAFLLOHVQE--LPVPALPTEARTCK						
Nod1	15	ESPEHQLKSNRELLVTHENTQ---QAVNDLKNDFPSAEAEIVCACTPT--PDQVRKILDAVOSKEEVSEFVLLOQ--LADAYMDLSPMLE						
RICK	434	-GLAQOQSKEEDIVNQTEACI--NOSDALISRDLMGEDVETKSTPR--TSKVRCLDITDIOGEFQVIVQIKQ--NKMGLOPYPEIIV						
ARC	6	-EPSETIDFERKGVETQCDSG---LLDALVARGVLTGTEPTEADAPD--ERRVRELLVQSKEBAQOELCAQOQVSPDPDPAWQVOP						
RAIDD	1	VEADQVIRSRILECAEVAIEG---LVLCVLYOEGILTEHIOENAOITG--FRKTMILLIDILPSROPADPTFDSLCERFVWEEKIKARBEAM						
Caspase-2	15	MPFHQETKQVRVLAQQLHIS---ELEHLEKQITTEPTELLQAKVS--SQNVELLNLPQROPADAFCEALRE--TQOGLDEMLITTL						
Ced-3	2	QODRSLEERNIMPSSEHMD---ELEHLEKQITTEPTELLQAKVS--SQNVELLNLPQROPADAFCEALRE--TQOGLDEMLITTL						
Ced-4	2	LCHECALSTHTRILLHDEPQ---DALVYLEGKNTTEDHSELISKVST--FEKRELVKAVORQDVADAFVDALES--TCEGLAEVIEREA						
Caspase-9	1	QDDERLRCKRERLVEBLQD---QMDVLISSEEDHPMEDIQAGSGSEDCARCLDITETRSQALFFICLED--TGODMLASFLRTN						
Apaf-1	1	MDKARNCILQHRBALEKDIKTS---KINDHMSDECLTISEEKVNEPTQ--QQAAMLIKMLIKONDSVVSFYNALLHESYKOLAALHDCIPV						
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B

Nod2	273	PATLG-----EELESTPGHNDADTVLVGPGSGKSTLIQRLHLLWAAGODFOELFVPP-----FSCROLOCWAKP--LSVRLLLPBH---CCMPDVGOEDIFQOLLDDHPD						
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C

Repeat 1	744	RSIEYEQEERUARKKARGNLVGHUKITP	α	β
Repeat 2	772	CSVGPTECAAFVYQHLRRFPVALQLDY		
Repeat 3	800	NSVGDIGVEQLPQ---GVCKALYLRD		
Repeat 4	825	NNISDRGIYKIECLHCEQLQKDALFN		
Repeat 5	853	NKUTDCAHSAKILACRONLALRLGN		
Repeat 6	881	NYITAGAQNVAEGRGNTSLQFLGNG		
Repeat 7	909	NRNGDEGAQDAEALGDHOSLRWLSVG		
Repeat 8	937	NNVGSVGAQADALMAKNVMEELCEE		
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Repeat 10	993	NCSTYLGAENLQALERNDTGLEWLRG		

Figure 2

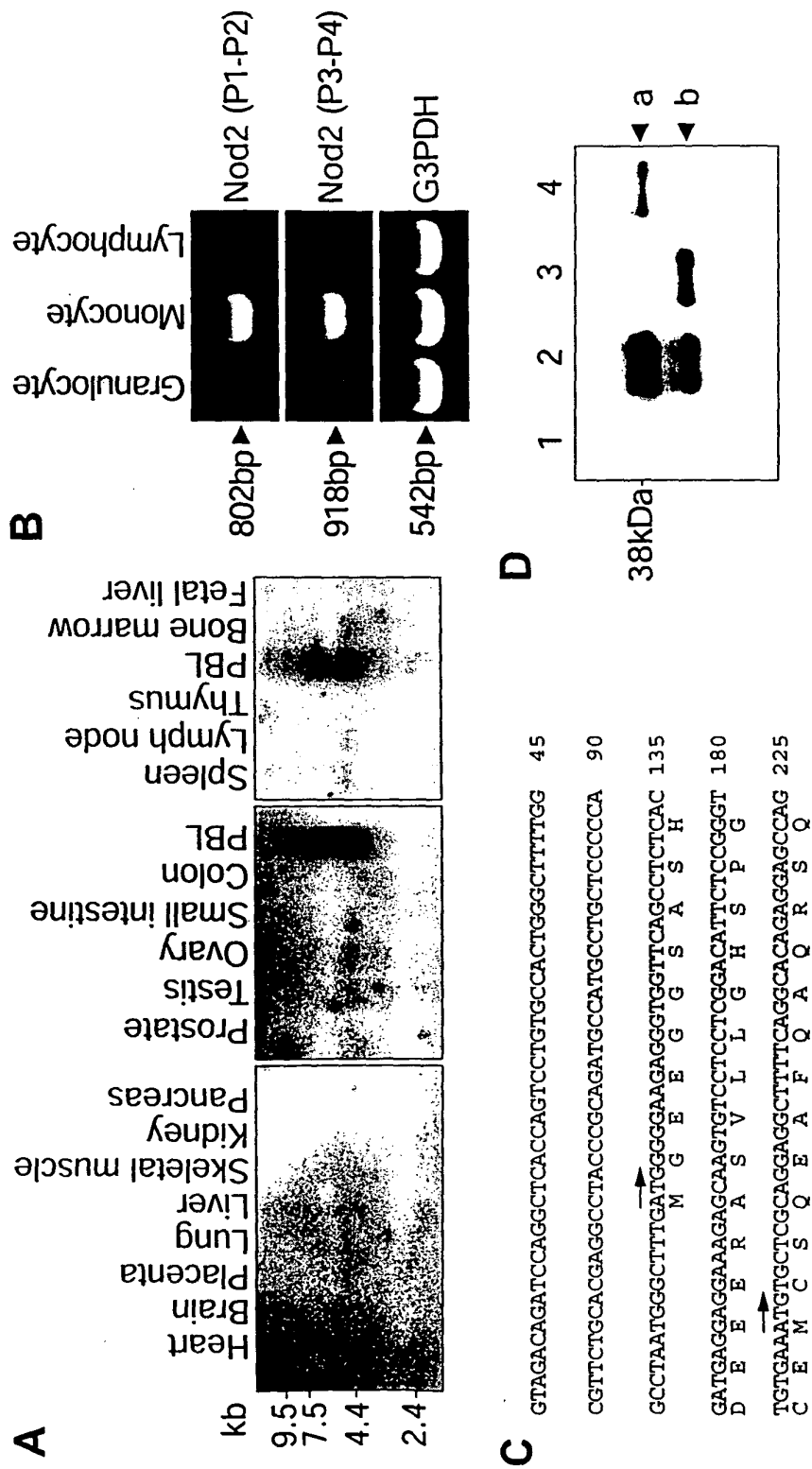


Figure 3

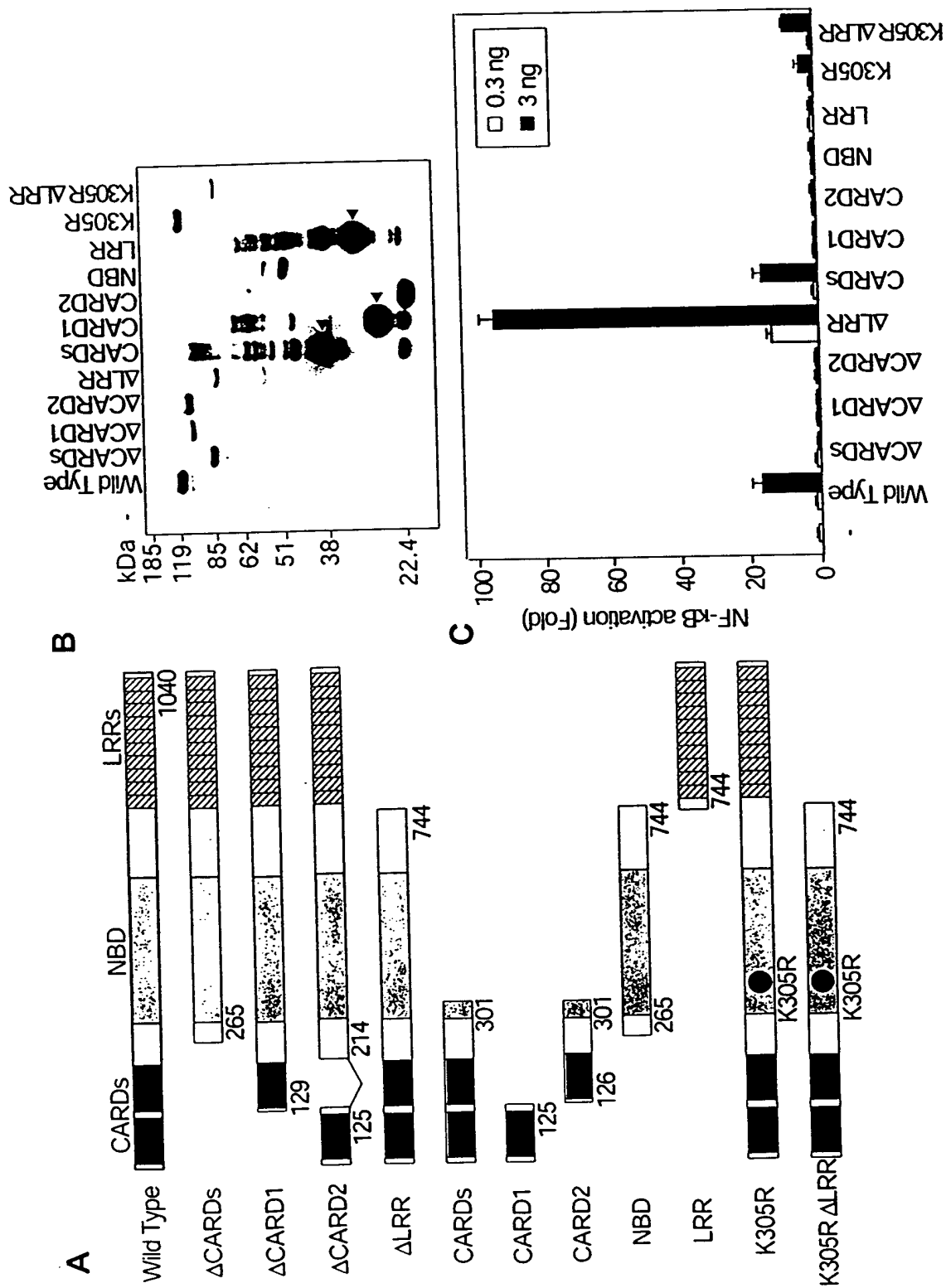


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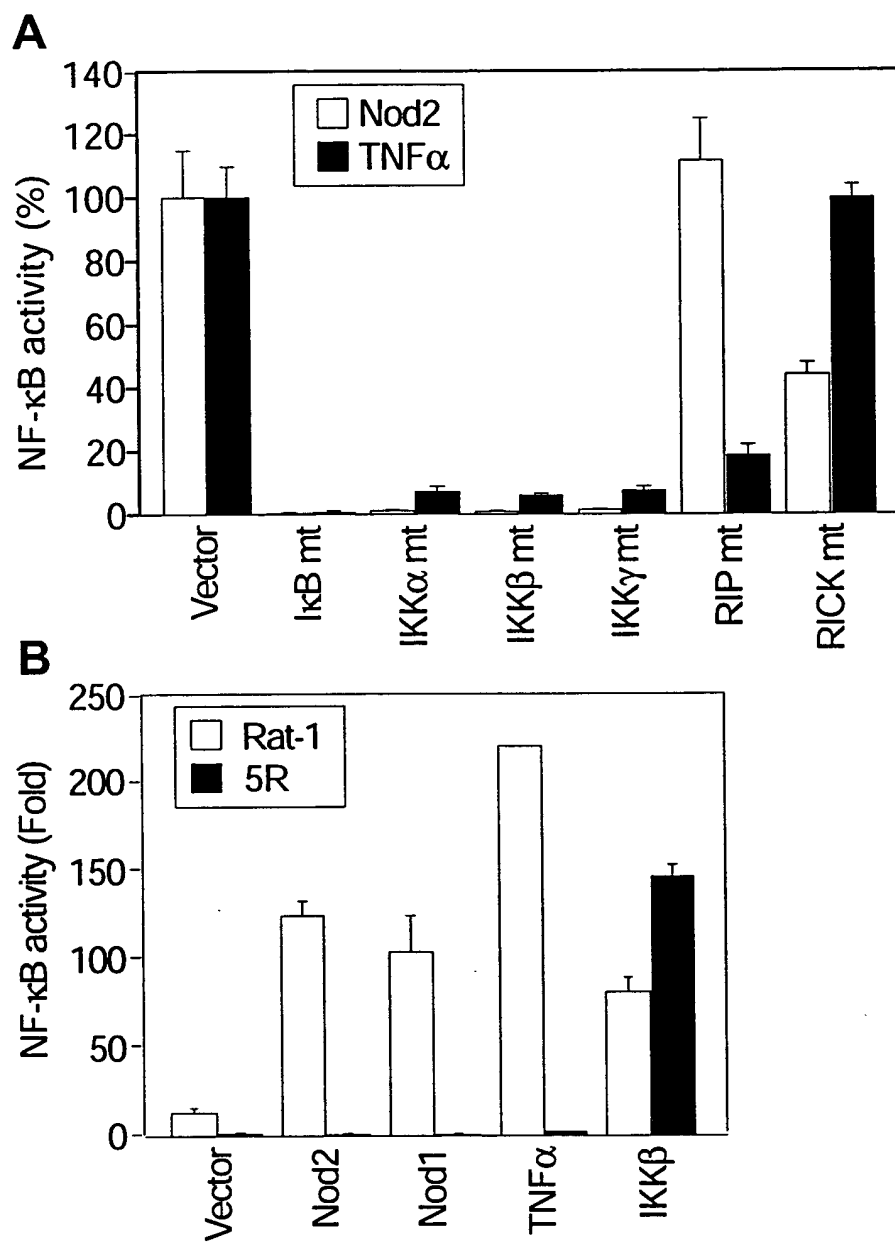


Figure 5

Figure 6

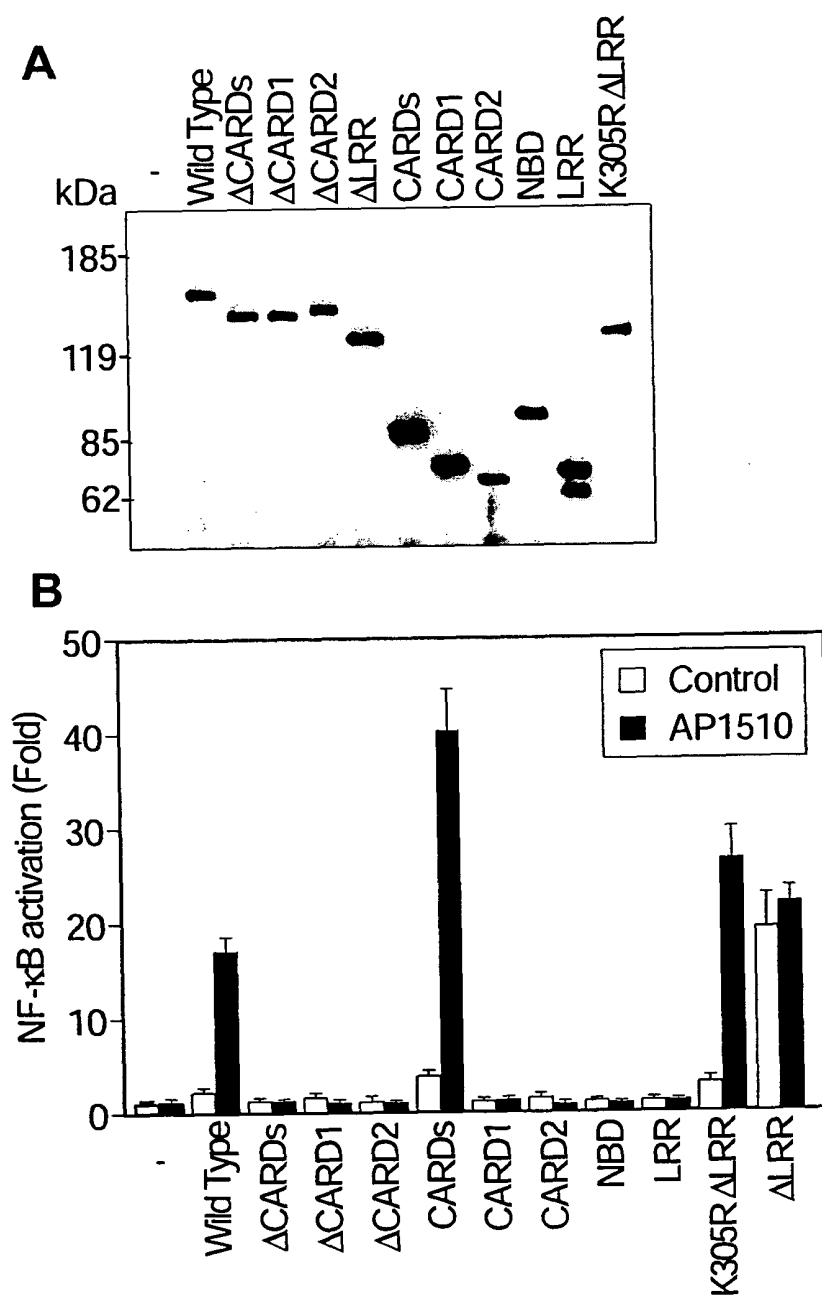


Figure 7

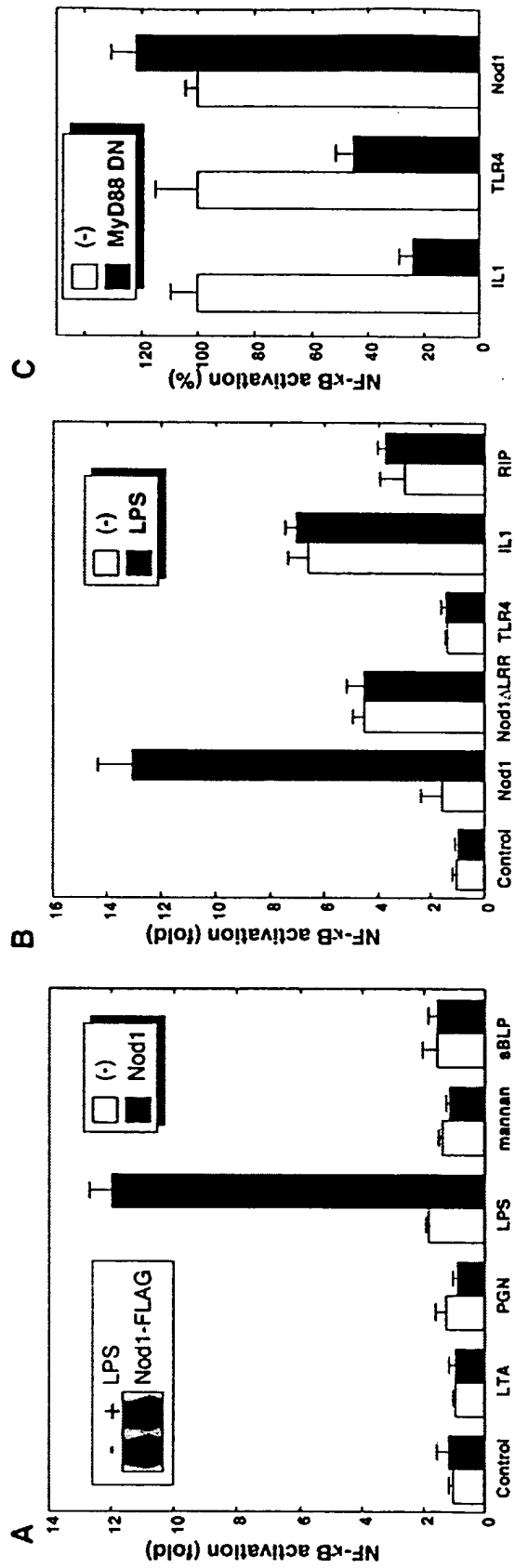


Figure 8

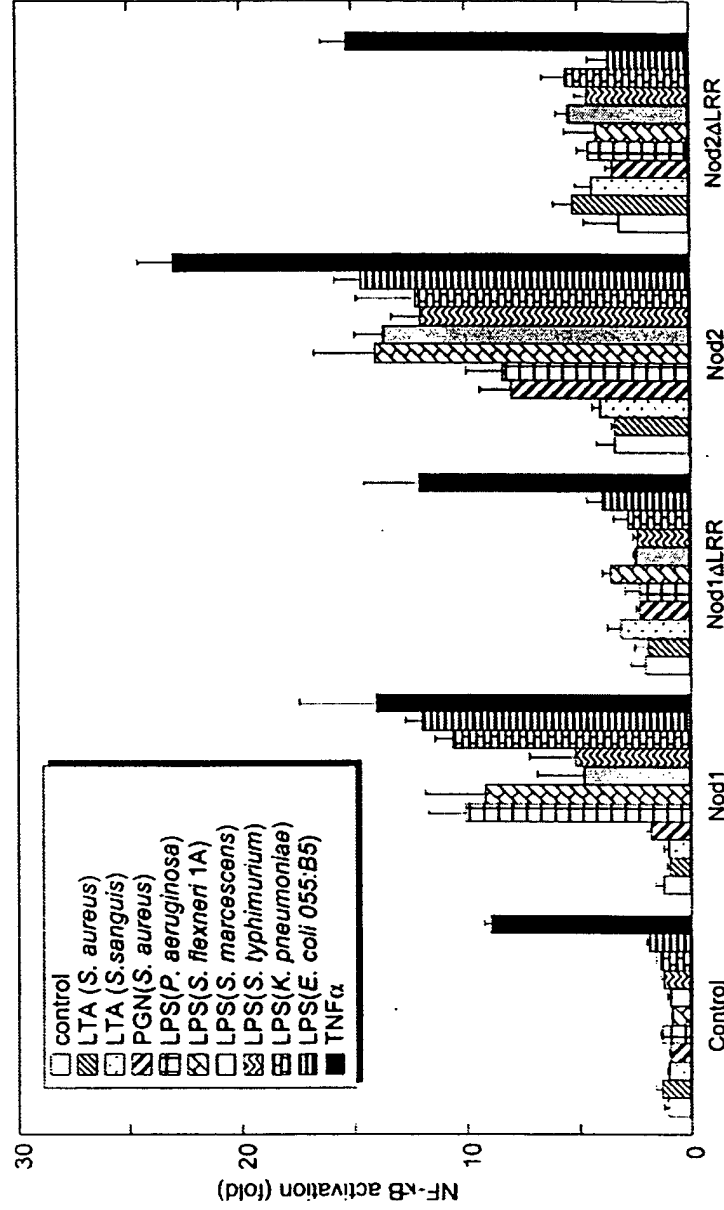


Figure 9

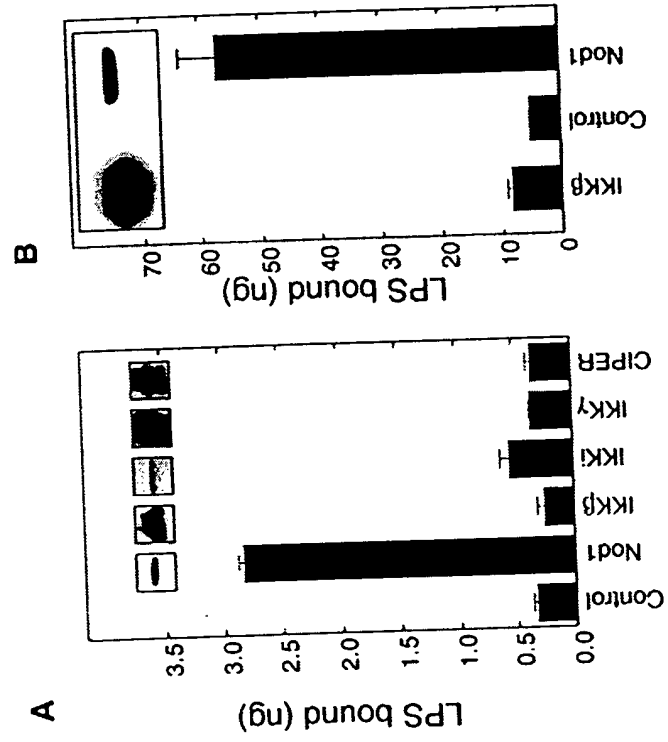


Figure 10

Figure 11

SEQ ID NO:33

Nod2 cDNA sequence

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Figure 12

SEQ ID NO:1

Nod2 cDNA sequence

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Figure 13

SEQ ID NO:2

MGEEGGSASH DEERASVLL GHSPGCEMCS QEAFQAQRSQ LVELLVSGSL EGFESVLDWL
LSWEVLSWED YEGFHLLGQP LSHLARRLLD TVWNKGTWAC QKLIAAAQEA QADSQSPKLH
GCWDPHSLHP ARDLQSHRPA IVRRLHSHVE NMLDLAWERG FVSQYECDEI RLPIFTSPQR
ARRLLDLATV KANGLAAFLD QHVQELPVPL ALPLEAATCK KYMAKLRTTV SAQSRFLSTY
DGAETLCLED IYTENVLEVW ADVGMAGPPQ KSPATLGLEE LFSTPGHLND DADTVLVVGE
AGSGKSTLLQ RLHLLWAAGQ DFQEFLFVFP FSCRQLQCMA KPLSVRTLLF EHCCWPDVGQ
EDIFQLLLDH PDRVLLTFDG FDEFKFRFTD RERHCSPTDP TSVQTLLFNL LQGNLLKNAR
KVVTSRPAAV SAFLRKYIRT EFNKGFSEQ GIELYLKRKH HEPGVADRLI RLLQETSALH
GLCHLPVFSW MVSCHQELL LQEGGSPKTT TDMYLLILQH FLLHATPPDS ASQGLGPSLL
RGRLPTLLHL GRLALWGLGM CCYVFSQQQL QAAQVSPDDI SLGFLVRAKG VVPGSTAPLE
FLHITFQCFE AAFYLALSAD VPPALLRHLF NCGRPGNSPM ARLLPTMCIQ ASEGKDSSVA
ALLQKAEPHN LQITAAFLAG LLSREHWGLL AECQTSEKAL LRRQACARWC LARSLRKHFH
SIPPAAPGEA KSVHAMPFI WLIRSLYEMQ EERLARKAAR GLNVGHLKLT FCSVGPTeca
ALAFVLQHLR RPVALQLDYN SVGDIGVEQL LPCLGVCKAL YLRDNNISDR GICKLIECAL
HCEQLQKLAL FNNKLTGCA HSMAKLLACR QNFLALRLGN NYITAAGAQQV LAEGLRGNTS
LQFLGFWGNR VGDEGAQALA EALGDHQLR WLSLVGNNIG SVGAQALALM LAKNVMLEEL
CLEENHLQDE GVCSLAELK KNSSLKILKL SNNCITYLGA EALLQALERN DTILEVWLRG
NTFSLEEVDK LGCRDTRLLL *

1004291022001

Figure 14

SEQ ID NO:3

MCSQEAFAQ RSQVLELLVS GSLEGFESVL DWLLSWEVLS WEDYEGFHLL GQPLSHLARR
LLDTVWNKGT WACQKLIAAA QEAQADSQSP KLHGCWDPHS LHPARDLQSH RPAIVRRLHS
HVENMLDLAW ERGFVSQYEC DEIRLPIFTP SQRARRLLDL ATVKANGLAA FLLQHVQELP
VPLALPLEAA TCKKYMALR TTVSAQSRFL STYDGAETLC LEDIYTENVL EVWADVGMAG
PPQKSPATLG LEELFSTPGH LNDDADTVLV VGEAGSGKST LLQRLHLLWA AGQDFQEFLE
VFPFSCRQLQ CMAKPLSVRT LLFEHCCWPD VGQEDIFQLL LDHPDRVLLT FDGFDEFKFR
FTDRERHCSP TDPTSVQTLN FNLLQGNLLK NARKVVTSRP AAVSAFLRKY IRTEFNLKGF
SEQGIELYLR KRHEPGVAD RLIRLLQETS ALHGLCHLPV FSWMVSKCHQ ELLQEGGSP
KTTTDMYLLI LQHFLHATP PDSASQGLGP SLLRGRLLPTL LHLGRLLALWG LGMCCYVFSA
QQLQAAQVSP DDISLGFLVR AKGVVPGSTA PLEFLHITFQ CFFAAFYLLAL SADVPPALLR
HLFNCGRPGN SPMARLLPTM CIQASEGKDS SVAALLQKAE PHNLQITAAL LAGLLSREHW
GLLAECQTSE KALLRRQACA RWCLARSLRK HFHSIPPAAP GEAKSVHAMP GFIWLIRSLY
EMQEERLARK AARGLNVGHL KLTFCSVGPT ECAALAFVLQ HLRRPVALQL DYNSVGDIGV
EQLLPCLGVC KALYLRDNNI SDRGICKLIE CALHCEQLQK LALFNNKLTG GCAHSMKLL
ACRQNFALR LGNNYITAAG AQVLAEGLRG NTSLQFLGFW GNRVGDEGAQ ALAEALGDHQ
SLRWLSLVGN NIGSVGAQAL ALMLAKNVML EELCLEENHL QDEGVCSLAE GLKKNSSLKI
LKLSNNCITY LGAEALLQAL ERNDTILEVW LRGNTFSLEE VDKLGCRDTR LLL*

100425.1000

Figure 15
SEQ ID NO:34

Nod2a AA sequence, Mutant

MGEEGGSASH DEEERASVLL GHSPGCEMCS QEAFQAQRSQ LVELLVSGSL EGFESVLDWL
LSWEVLSWED YEGFHLGQP LSHLARLLD TVWNKGTWAC QKLIAAAQEA QADSQSPKLH
GCWDPHSLHP ARDLQSHRPA IVRRLHSHVE NMLDLAWERG FVSQYECDEI RLPIFTSPQR
ARRLLDLATV KANGLAAFL L QHVQELPVPL ALPLEAATCK KYMAKLRTTV SAQSRFLSTY
DGAETLCLED IYTENVLEW ADVGMAGPPQ KSPATLGLEE LFSTPGHLND DADTVLVVGE
AGSGKSTLLQ RLHLLWAAGQ DFQEFLEFVP FSCRQLQCMA KPLSVRTLLEF EHCCWPDVGO
EDIFQLLLDH PDRVLLTFDG FDEFKFRFTD RERHCSPTDP TSVQTLLEFNL LQGNLLKNAR
KVVTSRPAAV SAFLRKYIRT EFNLKGFEQ GIELYLRKRH HEPGVADRLI RLLQETSALH
GLCHLPVFSW MVSCHQELL LQEGGSPKTT TDMYLLILQH FLLHATPPDS ASQGLGPSLL
RGRLPTLLHL GRLALWGLGM CCYVFSQQQL QAAQVSPDDI SLGFLVRAKG VVPGSTAPLE
FLHITFCFF AAFYLALSAD VPPALLRHLF NCGRPGNSPM ARLLPTMCIQ ASEGDSSVA
ALLQKAEPHN LQITAAFLAG LLSREHWGLL AECQTSEKAL LRRQACARWC LARSLRKHFH
SIPPAAPGEA KSVHAMPFI WLIRSLYEMQ EERLARKAAR GLNVGHLKLT FCSVGPTCA
ALAFVLQHLR RPVALQLDYN SVGDIGVEQL LPCLGVCKAL YLRDNNISDR GICKLIECAL
HCEQLQKLAL FNNKLTGCA HSMAKLLACR QNFLALRLGN NYITAAGAQQV LAEGLRGNTS
LQFLGFWGNR VGDEGAQALA EALGDHQLR WLSLVGNNIG SVGAQALALM LAKNVMLEEL
CLEENHLQDE GVCSLAELK KNSSLKILKL SNNCITYLGA EALLQAP*

10014259 "102501

FIGURE 16

Nod2 Exon11, Wild type

cagacatgag caggatgtgt ctaagggaca ggtgggcttc agtagactgg ctaactcctg

cagtctctttt aactggacag tttcaagagg aaaaccaaga atccttgaag ctcaccattg

tatcttctttt tccagGTTGT CCAATAACTG CATCACCTAC CTAGGGGCAG AAGCCCTCCT

L S N N C I T Y L G A E A L L

GCAGGCCCTT GAAAGGAATG ACACCATCCT GGAAGTCTGg taaggcccct gggcaggcct

Q A L E R N D T I L E V

gttttagctc tccgaacctc agtttttcta tctgtaaaat ggggtgacgg gagagaggaa

tggcagaatt ttgaggatcc cttctgattc tgacattcag tgagaatgat tctgcatgtg

Nod2 Exon11, Mutant

cagacatgag caggatgtgt ctaagggaca ggtgggcttc agtagactgg ctaactcctg

cagtctctttt aactggacag tttcaagagg aaaaccaaga atccttgaag ctcaccattg

tatcttctttt tccagGTTGT CCAATAACTG CATCACCTAC CTAGGGGCAG AAGCCCTCCT

L S N N C I T Y L G A E A L L

GCAGGCCCTT TGAAAGGAAT GACACCATCC TGAAGTCTG gtaaggcccc tgggcaggcc

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Q A P *

tgtttttagct ctccgaacct cagtttttct atctgtaaaa tggggtgacg ggagagagga

atggcagaat ttgaggatc ccttctgatt ctgacattca gtgagaatga ttctgcatgt

g

10014269.102601
102601.632400